REMARKS

Claims 1-53 are pending in the application. Claims 28-49 and 51-53 have been withdrawn. Claims 1-4 and 6-8 have been amended. Favorable reconsideration of the application, as amended, is respectfully requested.

SEQUENCE RULES

The Examiner states that in order to comply with the sequence rules, Applicants must identify the sequence by providing SEQ ID NO, and where required provide a new version of the sequence listing and disk. If the primer nucleotide sequence is already part of the sequence listing and the CRF, Applicants may amend the specification by providing the appropriate SEQ ID NO:, following the sequence.

Applicants have amended the specification to include the SEQ ID NOs to identify the sequences recited within the specification.

CLAIM OBJECTIONS

Claims 1-12, 22-25 have been objected to because of the following informalities: These claims depend upon or recite non-elected subject matter which must be deleted.

Applicants respectfully submit that Applicants are entitled to retain in the application claims to the nonelected species, where the requirement for restriction is predicated upon the nonallowability of generic claims. MPEP §809.02. The Examiner has indicated that claims 1-6, 28-33 and 50 are generic.

ALLOWABLE CLAIM

The Examiner has indicated that claim 50 is allowable.

I. REJECTION OF CLAIMS 1-12 AND 22-26 UNDER 35 U.S.C. § 112

Claims 1-12 and 22-26 have been rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Specifically, claims 6-8 recite the phrase "is derived from". The Examiner suggests amending the claims to recite "is

obtained from" in order to overcome this rejection. Applicants have amended claims 6-8 as suggested by the Examiner.

The Examiner has rejected claim 1 as being indefinite for reciting motif sequence 1 without the actual sequence identifier. Identifying the motif sequence 1 and including at the end of the sequence (SEQ ID No: 25) is suggested to overcome the rejection. Claims 2-12 and 22-26 are included in the rejection for failing to correct the defect present in the base claim(s). Applicants have amended claim 1 to include the SEQ ID NOs.

Claims 2-3 have been rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. It is the Examiner's position that the specification only provides description of a single species of sucrose phosphorylase (SEQ ID NO: 2 from *Steptococcus mutans)* and 8 mutants thereof (claim 50). Additional modifications of the sequence motif 1 (SEQ ID NO: 25) at positions 14, 29 and 44 are also disclosed. The Examiner contends that the specification does not contain any disclosure or description of the structure and function of all amino acid sequences that are at least 40% or 60% identical to SEQ ID NO: 2.

Applicants respectfully traverse the rejection for at least the following reasons. Claim 2 has been amended to recite that the amino acid sequence of the natural sucrose phosphorylase has at least *60%* identity with an amino acid sequence selected from the group consisting of *SEQ ID NO: 2.* Claim 3 has been amended to recite that the amino acid sequence of the natural sucrose phosphorylase has at least *70%* identity with an amino acid sequence selected from the group consisting of *SEQ ID NO: 2.* Support for the amendment can be found in the specification at least at page 74, line 16 to page 75, line 12 (paragraphs [0304]-[0305] of the US published application).

Motif sequences 1, 2, and 3 are highly conserved between multiple sucrose phosphorylases. Amino acid sequences at the position corresponding to the motif sequence 1, 2 or 3 for 10 sucrose phosphorylase shown in Figure 1A and 1B has 66%

or more amino acid identity to motif sequence 1, 2 or 3, respectively. The calculated results are shown in the following table:

	Identity compared to			
	motif sequence 1[*1]	motif sequence 2[*2]	motif sequence 3[*3]	SEQ ID NO:2[*4]
Streptococcus mutans (StMuSP)	100	100	100	100.0
Streptococcus pneumonia (StPSP)	91	93	89	83.8
Streptococcus sorbinus (StSSP)	89	83	89	82.5
Streptococcus mitis (StMiSP)	93	93	89	84.7
Leuconostoc mesentroides 1 (LeuSP1)	84	83	76	65.9
Leuconostoc mesentroides 2 (LeuSP2)	80	88	74	66.2
Oenococcus oeni (OenSP)	80	81	66	65.0
Lactobacillus acidophilus 1 (LBSP1)	66	69	79	63.6
Lactobacillus acidophilus 2 (LBSP2)	79	79	82	72.1
Listeria monocytogenes (ListMSP)	79	74	84	68.8

*1 Partial amino acid sequence of each of the sucrose phosphorylases corresponding to motif sequence 1 is compared to motif sequence 1.
*2 Partial amino acid sequence of each of the sucrose phosphorylases corresponding to motif sequence 2 is compared to motif sequence 2.
*3 Partial amino acid sequence of each of the sucrose phosphorylases corresponding to motif sequence 3 is compared to motif sequence 3.
*4 Full length amino acid sequence of each of the sucrose phosphorylases was compared to amino acid sequence NO: 2.

In each of the motif sequences, the similarity of the partial amino acid sequences corresponding to motif sequence 1, 2 or 3 to motif sequence 1, 2 or 3 are higher than the similarity of the full length amino acid sequence to SEQ ID NO: 2. These high degrees of similarity indicate that these motif sequences are highly conserved between the amino acid sequences of sucrose phosphorylases. Those skilled in the art would easily understand that these motif sequences have a common function or effect.

As shown in Tables 4A and 4B, substitution of amino acid residues at position 14, 29 or 44 of motif sequence 1, at position 7, 19, 23 or 34 of motif sequence 2, or at position 19 of motif sequence 3 of *Streptococcus mutans* improved thermostability. Thus, those skilled in the art would easily understand that these positions relate to the

improvement of thermostability of sucrose phosphorylase, and that substitution of amino acid residues at the same positions in other sucrose phosphorylases would improve the thermostability of the sucrose phosphorylase.

Furthermore, the amino acid residue at position 29 of motif sequence 1 is serine in *Streptococcus mutans*-derived sucrose phosphorylase, and is alanine in *Leuconostoc mesenteroides*-derived sucrose phosphorylase. Substitutions of this serine and alanine improved thermostability of these sucrose phosphorylases. This means that what amino acid residue is present in this position of the natural sucrose phosphorylase is not important. This means that the positions relating to improvement of thermostability and amino acid residue after substitution are important.

The high degrees of identity indicate between these motif sequences show such are highly conserved between the amino acid sequences of sucrose phosphorylases. Thus, those skilled in the art would easily understand that these motif sequences have a common function or effect. As such, even the effects of the un-exemplified modifications in positions 47, 77, 140, 144 and 249 could easily be understood as being similar to those in the 3 exemplified positions. As the 5 positions are highly conserved in motif sequences 1-3, as shown in Figures 1A-1C, conformation and biological characteristics thereof would easily be predictable to one skilled in the art.

Furthermore, the *Leuconostoc mesenteroides*-derived sucrose phosphorylase (LeuSP1) used in Example 2C, at page 155, lines 9-17 (paragraph [0514] of the US published application), shares 65.9% identity with SEQ ID NO: 2 of *streptococcus mutans*-derived sucrose phosphorylase and contrary to having one of the lower similarity shown in the above table, modification of LeuSP1 revealed the desired improved thermostability. In view of the foregoing, the specification as filed provides ample detail for the invention of amended claims 2 and 3, wherein the sequence homology is at least 60% or 70% identical to SEQ ID NO: 2.

Claims 2-4 have been rejected under 35 U.S.C. § 112, first paragraph. It is the Examiner's position that the specification, while being enabling for sucrose phosphorylase sequence of SEQ ID NO: 2, does not reasonably provide enablement

for any protein sequence having at least 40% or 60% homology to SEQ ID NO: 2 and which has the biological activity of a sucrose phosphorylase which amounts to a sequence by insertion, deletion or substitution, and having the biological activity of a sucrose phosphorylase.

Applicants respectfully traverse the rejection for at least the following reasons. As discussed above, claim 2 has been amended to recite that the amino acid sequence of the natural sucrose phosphorylase has at least *60%* identity with an amino acid sequence selected from the group consisting of *SEQ ID NO: 2.* Claim 3 has been amended to recite that the amino acid sequence of the natural sucrose phosphorylase has at least *70%* identity with an amino acid sequence selected from the group consisting of *SEQ ID NO: 2*. Applicants respectfully submit that the specification provides enablement for any protein sequence having at least 40% or 60% homology to SEQ ID NO: 2, as explained above.

With regard to claim 4, Applicants have amended claim 4 to recite the conditions under which hybridization is performed. Support for the amendment can be found in the specification at least at page 75, line 33 to page 76, line 19 (paragraph [0307] of the US published application). In view of the amendments and the forgoing remarks, Applicants respectfully submit that the rejections under 35 U.S.C. §112 have been overcome.

II. CONCLUSION

Accordingly, claims 1-27 and 50 are believed to be allowable and the application is believed to be in condition for allowance. A prompt action to such end is earnestly solicited.

Should the Examiner feel that a telephone interview would be helpful to facilitate favorable prosecution of the above-identified application, the Examiner is invited to contact the undersigned at the telephone number provided below.

Should a petition for an extension of time be necessary for the timely reply to the outstanding Office Action (or if such a petition has been made and an additional

extension is necessary), petition is hereby made and the Commissioner is authorized to charge any fees (including additional claim fees) to Deposit Account No. 18-0988.

Respectfully submitted,

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